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Docket No: 04983-0207.00US00/38-10(15498)A

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of Yongwei Cao *et al.*

Art Unit: 1656

Serial No: 09/404,520

Examiner: Strzelecka

Filed : September 23, 1999

For: *Emericella nidulans* Genome
and Uses Thereof

March 30, 2001

9/a
180
4/7/01RESPONSE TO RESTRICTION REQUIREMENT
AND PRELIMINARY AMENDMENT

Assistant Commissioner for Patents

Washington, DC 20231

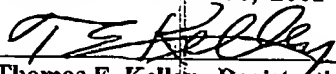
Sir:

The Office Action mailed February 12, 2001 sets forth an 11 way restriction requirement. Applicants respectfully traverse and submit that, because the restricted claims recite common nucleic or amino acid sequences, a common search would not be burdensome. Regardless, applicants provisionally elect the subject matter of Group XI comprising original claims 29 and 30 and new dependent claims added by amendment below.

Applicants also traverse the requirement to elect a single nucleic acid sequence. Independent claim 29 is directed to "computer readable medium having recorded thereon *at least 100* of the nucleotide sequences depicted in SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof." A restriction to a single nucleotide sequence prevents the claimed invention of *at least 100* sequences from ever being examined.

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Thomas E. Kelley, Registration No. 29,938

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Although applicants believe that the claimed invention should be examined without a sequence restriction, applicants provisionally elect a 100 nucleotide sequence set (SEQ ID NO: 16207 through 16306) and a single sequence (SEQ ID NO: 16207).

Because the restriction to a single nucleotide sequence prevents the examination of applicants' claimed invention, the undersigned respectfully requests an interview to discuss the single sequence restriction.

PRELIMINARY AMENDMENT

Please enter the following preliminary amendment to claims 29 and 30 and add new claims 47-58:

-- 29. (Amended) Computer readable medium having recorded thereon at least 100 of the nucleotide sequences [depicted in] selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 [or] and complements thereof. --

-- 30. (Amended) Computer readable medium according to claim 29, having recorded thereon at least 1000 of said nucleotide sequences. --

-- 47. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 26804 and complements thereof. --

-- 48. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 25999 and complements thereof. --

-- 49. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 24034 and complements thereof. --

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- 50. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 22709 and complements thereof. --
- 51. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17680 and complements thereof. --
- 52. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17617 complements thereof. --
- 53. Computer readable medium of claim 29 wherein said nucleotide sequences are selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17294 and complements thereof. --
- 54. Computer readable medium comprising the nucleotide sequences of the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 26804. --
- 55. Computer readable medium of claim 29 which is adapted for homology searching of nucleotide sequence.--
- 56. Computer readable medium of claim 55 wherein said medium is adapted for homology searching using a BLAST algorithm.--
- 57. A computer based system comprising computer readable medium of claim 29, input means for receiving a target sequence, means for identifying fragments of sequence recorded in said computer readable medium which are homologous to a target sequence, and an output means for outputting identified homologous sequences.--
- 58. A method of identifying nucleotide sequence comprising comparing target sequence to a sequence stored in computer readable medium of claim 29.--

While original claims 29 and 30 are believed to be patentable, the amendment to claims 29-30 serves to better encompass the full scope and breadth of the invention. New

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claims 47-58 are dependent from claim 29 and are supported by specification as filed. For instance, the subsets of recorded sequence in new claims 47-54 are found in the subsets of original claims 2-8; the homology searching limitations in new claims 55-56 are found in the specification at pages 37-39; computer based systems of new claim 57 is found at pages 38-39 and methods of identifying nucleotide sequence using the medium in new claim 58 is found at page 38.

Respectfully submitted,



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GENOMICS

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GROUP 1600

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CAMBRIDGE, MA 02139

DATE March 30, 2001
TO Assistant Commissioner for Patents
Attention: Examiner Strzelecka at Art Unit: 1656
FAX 703-308-4242
FROM Thomas E. Kelley, Reg. No. 29,938
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CC
SUBJECT Response in Serial No. 09/404,520
PAGES 5 including this cover sheet

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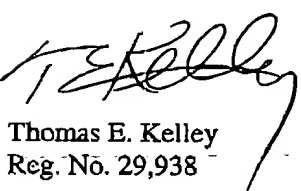
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Enclosed is a Response to Restriction Requirement and Preliminary Amendment in
application Serial No. 09/404,520


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